FIGURE 1A

```
ATG GGG TGG CTT TGC TCT GGG CTC CTG TTC CCT GTG AGC TGC CTG -31
Met Gly Trp Leu Cys Ser Gly Leu Leu Phe Pro Val Ser Cys Leu -11

GTC CTG CTG CAG GTG GCA AGC TCT GGG AAC ATG AAG GTC TTG CAG  15
Val Leu Leu Gln Val Ala Ser Ser Gly Asn Met Lys Val Leu Gln   5

GAG CCC ACC TGC GTC TCC GAC TAC ATG AGC ATC TCT ACT TGC GAG  60
Glu Pro Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu  20

TGG AAG ATG AAT GGT CCC ACC AAT TGC AGC ACC GAG CTC CGC CTG 105
Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu  35

TTG TAC CAG CTG GTT TTT CTG CTC TCC GAA GCC CAC ACG TGT ATC 150
Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile  50

CCT GAG AAC AAC GGA GGC GCG GGG TGC GTG TGC CAC CTG CTC ATG 195
Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu Met  65

GAT GAC GTG GTC AGT GCG GAT AAC TAT ACA CTG GAC CTG TGG GCT 240
Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala  80

GGG CAG CAG CTG CTG TGG AAG GGC TCC TTC AAG CCC AGC GAG CAT 285
Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His  95

GTG AAA CCC AGG GCC CCA GGA AAC CTG ACA GTT CAC ACC AAT GTC 330
Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val 110

TCC GAC ACT CTG CTG CTG ACC TGG AGC AAC CCG TAT CCC CCT GAC 375
Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp 125

AAT TAC CTG TAT AAT CAT CTC ACC TAT GCA GTC AAC ATT TGG AGT 420
Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser 140

GAA AAC GAC CCG GCA GAT TTC AGA ATC TAT AAC GTG ACC TAC CTA 465
Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu 155

GAA CCC TCC CTC CGC ATC GCA GCC AGC ACC CTG AAG TCT GGG ATT 510
Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile 170

TCC TAC AGG GCA CGG GTG AGG GCC TGG GCT CAG TGC TAT AAC ACC 555
Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr Asn Thr 185

ACC TGG AGT GAG TGG AGC CCC AGC ACC AAG TGG CAC AAC TCC TAC 600
Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr 200

AGG GAG CCC TTC GAG CAG CAC CTC CTG CTG GGC GTC AGC GTT TCC 645
Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser 215

TGC ATT GTC ATC CTG GCC GTC TGC CTG TTG TGC TAT GTC AGC ATC 690
Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile 230

ACC AAG ATT AAG AAA GAA TGG TGG GAT CAG ATT CCC AAC CCA GCC 735
Thr Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala 245
```

FIGURE 1B

```
CGC AGC CGC CTC GTG GCT ATA ATA ATC CAG GAT GCT CAG GGG TCA  780
Arg Ser Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser  260

CAG TGG GAG AAG CGG TCC CGA GGC CAG GAA CCA GCC AAG TGC CCA  825
Gln Trp Glu Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro  275

CAC TGG AAG AAT TGT CTT ACC AAG CTC TTG CCC TGT TTT CTG GAG  870
His Trp Lys Asn Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu  290

CAC AAC ATG AAA AGG GAT GAA GAT CCT CAC AAG GCT GCC AAA GAG  915
His Asn Met Lys Arg Asp Glu Asp Pro His Lys Ala Ala Lys Glu  305

ATG CCT TTC CAG GGC TCT GGA AAA TCA GCA TGG TGC CCA GTG GAG  960
Met Pro Phe Gln Gly Ser Gly Lys Ser Ala Trp Cys Pro Val Glu  320

ATC AGC AAG ACA GTC CTC TGG CCA GAG AGC ATC AGC GTG GTG CGA 1005
Ile Ser Lys Thr Val Leu Trp Pro Glu Ser Ile Ser Val Val Arg  335

TGT GTG GAG TTG TTT GAG GCC CCG GTG GAG TGT GAG GAG GAG GAG 1050
Cys Val Glu Leu Phe Glu Ala Pro Val Glu Cys Glu Glu Glu Glu  350

GAG GTA GAG GAA GAA AAA GGG AGC TTC TGT GCA TCG CCT GAG AGC 1095
Glu Val Glu Glu Glu Lys Gly Ser Phe Cys Ala Ser Pro Glu Ser  365

AGC AGG GAT GAC TTC CAG GAG GGA AGG GAG GGC ATT GTG GCC CGG 1140
Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu Gly Ile Val Ala Arg  380

CTA ACA GAG AGC CTG TTC CTG GAC CTG CTC GGA GAG GAG AAT GGG 1185
Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly Glu Glu Asn Gly  395

GGC TTT TGC CAG CAG GAC ATG GGG GAG TCA TGC CTT CTT CCA CCT 1230
Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu Leu Pro Pro  410

TCG GGA AGT ACG AGT GCT CAC ATG CCC TGG GAT GAG TTC CCA AGT 1275
Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe Pro Ser  425

GCA GGG CCC AAG GAG GCA CCT CCC TGG GGC AAG GAG CAG CCT CTC 1320
Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro Leu  440

CAC CTG GAG CCA AGT CCT CCT GCC AGC CCG ACC CAG AGT CCA GAC 1365
His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp  455

AAC CTG ACT TGC ACA GAG ACG CCC CTC GTC ATC GCA GGC AAC CCT 1410
Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro  470

GCT TAC CGC AGC TTC AGC AAC TCC CTG AGC CAG TCA CCG TGT CCC 1455
Ala Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro  485

AGA GAG CTG GGT CCA GAC CCA CTG CTG GCC AGA CAC CTG GAG GAA 1500
Arg Glu Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu  500

GTA GAA CCC GAG ATG CCC TGT GTC CCC CAG CTC TCT GAG CCA ACC 1545
Val Glu Pro Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr  515
```

FIGURE 1C

```
ACT GTG CCC CAA CCT GAG CCA GAA ACC TGG GAG CAG ATC CTC CGC 1590
Thr Val Pro Gln Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg  530

CGA AAT GTC CTC CAG CAT GGG GCA GCT GCA GCC CCC GTC TCG GCC 1635
Arg Asn Val Leu Gln His Gly Ala Ala Ala Ala Pro Val Ser Ala  545

CCC ACC AGT GGC TAT CAG GAG TTT GTA CAT GCG GTG GAG CAG GGT 1680
Pro Thr Ser Gly Tyr Gln Glu Phe Val His Ala Val Glu Gln Gly  560

GGC ACC CAG GCC AGT GCG GTG GTG GGC TTG GGT CCC CCA GGA GAG 1725
Gly Thr Gln Ala Ser Ala Val Val Gly Leu Gly Pro Pro Gly Glu  575

GCT GGT TAC AAG GCC TTC TCA AGC CTG CTT GCC AGC AGT GCT GTG 1770
Ala Gly Tyr Lys Ala Phe Ser Ser Leu Leu Ala Ser Ser Ala Val  590

TCC CCA GAG AAA TGT GGG TTT GGG GCT AGC AGT GGG GAA GAG GGG 1815
Ser Pro Glu Lys Cys Gly Phe Gly Ala Ser Ser Gly Glu Glu Gly  605

TAT AAG CCT TTC CAA GAC CTC ATT CCT GGC TGC CCT GGG GAC CCT 1860
Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly Cys Pro Gly Asp Pro  620

GCC CCA GTC CCT GTC CCC TTG TTC ACC TTT GGA CTG GAC AGG GAG 1905
Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly Leu Asp Arg Glu  635

CCA CCT CGC AGT CCG CAG AGC TCA CAT CTC CCA AGC AGC TCC CCA 1950
Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser Ser Ser Pro  650

GAG CAC CTG GGT CTG GAG CCG GGG GAA AAG GTA GAG GAC ATG CCA 1995
Glu His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp Met Pro  665

AAG CCC CCA CTT CCC CAG GAG CAG GCC ACA GAC CCC CTT GTG GAC 2040
Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val Asp  680

AGC CTG GGC AGT GGC ATT GTC TAC TCA GCC CTT ACC TGC CAC CTG 2085
Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu  695

TGC GGC CAC CTG AAA CAG TGT CAT GGC CAG GAG GAT GGT GGC CAG 2130
Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln  710

ACC CCT GTC ATG GCC AGT CCT TGC TGT GGC TGC TGC TGT GGA GAC 2175
Thr Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp  725

AGG TCC TCG CCC CCT ACA ACC CCC CTG AGG GCC CCA GAC CCC TCT 2220
Arg Ser Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser  740

CCA GGT GGG GTT CCA CTG GAG GCC AGT CTG TGT CCG GCC TCC CTG 2265
Pro Gly Gly Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu  755

GCA CCC TCG GGC ATC TCA GAG AAG AGT AAA TCC TCA TCA TCC TTC 2310
Ala Pro Ser Gly Ile Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe  770

CAT CCT GCC CCT GGC AAT GCT CAG AGC TCA AGC CAG ACC CCC AAA 2355
His Pro Ala Pro Gly Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys  785

ATC GTG AAC TTT GTC TCC GTG GGA CCC ACA TAC ATG AGG GTC TCT 2400
Ile Val Asn Phe Val Ser Val Gly Pro Thr Tyr Met Arg Val Ser  800
```

Figure 2A

```
                                        FR1
L1   1   GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA AAGAGCCACC  60
L2   1   GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA AAGAGCCACC  60
L3   1   GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCGGGGGA AAGAGCCACC  60
L4   1   GAAATTGTGA TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA AAGAGCCACC  60
L5   1   GATATTGTGC TGACCCAGTC TCCAGCCACC CTGTCTTTGT CTCCAGGGGA AAGAGCCACC  60
L6   1   GATATTGTGC TGACGCAGAC TCCAGCCACC CTGTCTTTGT CTCCAGGGGA AAGAGCCACC  60

                                       CDR1
L1  61   CTCTCCTGCA GGGCCAGTCA GAGTGTTAGC AGCAGCTACT TAGCCTGGTA CCAGCAGAAA  120
L2  61   CTCTCCTGCA GGGCCAGTCA GAGTGTTAGC AACAGCTACT TAGCCTGGTA CCAGCAGAAA  120
L3  61   CTCTCCTGCA GGGCCAGTCA GACTGTTAAC AGCGACTACT TAGCCTGGTA CCAGCAGAAA  120
L4  61   CTCTCCTGCA GGGCCAGTCA GAGTGTTAGC AGCGACTACT TAGCCTGGTA CCAGCAGAAA  120
L5  61   CTCTCCTGCA GGGCCAGTCA GAGTGTTAAC AGCAACTACT TAGCCTGGTA CCAGCAGAAA  120
L6  61   CTCTCCTGCA GGGCCAGTCA GAGTGTTGGC AGCAGCTACT TAGCCTGGTA CCAGCAGAGA  120

                 FR2                                CDR2
L1 121 CCTGGCCAGG CTCCCAGGCT CCTCATCTTT GGTGCATCCA GCAGGGCCAC TGGCATCCCA  180
L2 121 CCTGGCCAGG CTCCCAGGCT CCTCATCTAT GGTGCATCCA GCAGGGCCCC TGGCATCCCA  180
L3 121 CCGGGCCAGG CTCCCAGGCT CCTCATCTAT GGTGCATCCA GCAGGGCCAC TGGCATCCCA  180
L4 121 CCTGGCCAGG CTCCCAGGCT CCTCATCTAT GGTGCATCTA GCAGGGCCTC TGGCATCCCA  180
L5 121 CCTGGCCAGG CTCCCAGGCT CCTCATCTAT GGTACATCCT ACAGGGCCAC TGGCATCCCA  180
L6 121 CCTGGCCAGG CTCCCAGGCT CCTCATCTAT GGTGCATCCA GCAGGGCCAC TGGCATCCCG  180

                                      FR3
L1 181 GACAGGTTCA GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG  240
L2 181 GACAGGTTCA GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG  240
L3 181 GACAGGTTCA GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG  240
L4 181 GACAGGTTCA GTGGCAGTGG GTTTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG  240
L5 181 GACAGGTTCA GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAC CAGACTGGAG  240
L6 181 GACAGGTTCA GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACGATCAG CAGACTGGAG  240

                                                 CDR3
L1 241 CCTGAAGATT TTGCAGTGTA TTACTGTCAG CAGTATGGTA GCTCACCTCC GTGGACGTTC  300
L2 241 CCTGAAGATT TTGCAGTGTA TTACTGTCAG CAGTATGATC ACTCAGCAGG GTGGACGTTC  300
L3 241 CCTGAAGATT TTGCAGTCTA TTACTGTCAG CAGTATGGTA GGTCACCTCC GTGGACGTTC  300
L4 241 CCTGAAGATT TTGCAATATA TTACTGTCAG CAGTATGGTA GCTCACCTCC GTGGACGTTC  300
L5 241 CCTGAAGATT TTGCAGTGTA TTACTGTCAG CAGTATGGTA GCTCACCACC GTGGACGTTC  300
L6 241 CCTGAAGATT TTGCAGTGTA TTATTGTCAG CAGTATGGAA GTTCACCTCC GTGGATGTTC  300

                 FR4
L1 301 GGCCAAGGGA CCAAGGTGGA AATCAAA  327
L2 301 GGCCAAGGGA CCAAGGTGGA GATCAAA  327
L3 301 GGCCAAGGGA CCAAAGTGGA TATCAAA  327
L4 301 GGCCAAGGGA CCAAGGTGGA AATCAAA  327
L5 301 GGCCAAGGGA CACGACTGGA GATTAAA  327
L6 301 GGCCAAGGGA CCAAGGTGGA GATCAAA  327
```

Figure 2B

FR1

H1	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H2	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H3	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H4	1	GAGGTTCAGT	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H5	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H6	1	GAGGTTCAGT	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H7	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H8	1	GAGGTTCAGT	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H9	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H10	1	GAGGTTCAGT	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H11	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H12	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H13	1	GAGGTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGTC	CCTGAGACTC	60
H14	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60
H15	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60
H16	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60
H17	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60
H18	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60
H19	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60
H20	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60
H21	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60
H22	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60
H23	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60
H24	1	GAGGTTCAGT	TGGTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGTC	CCTGAGACTC	60

CDR1

H1	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H2	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H3	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H4	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H5	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H6	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H7	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H8	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H9	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H10	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H11	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H12	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H13	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H14	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H15	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H16	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H17	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H18	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H19	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H20	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H21	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H22	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H23	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120
H24	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	**AGAAATGCTA**	**TGTTC**TGGGT	TCGCCAGGCT	120

Figure 2C

		FR2			CDR2		
H1	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAACTATGCA** 180
H2	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H3	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H4	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAACTATGCA** 180
H5	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAACTATGCA** 180
H6	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAACTATGCA** 180
H7	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H8	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAACTATGCA** 180
H9	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H10	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAACTATGCA** 180
H11	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H12	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H13	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H14	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H15	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H16	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H17	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H18	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H19	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H20	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H21	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H22	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H23	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180
H24	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCA**GGT**	**ATTGGTACTG**	**GTGGTGCCAC**	**AAGCTATGCA** 180

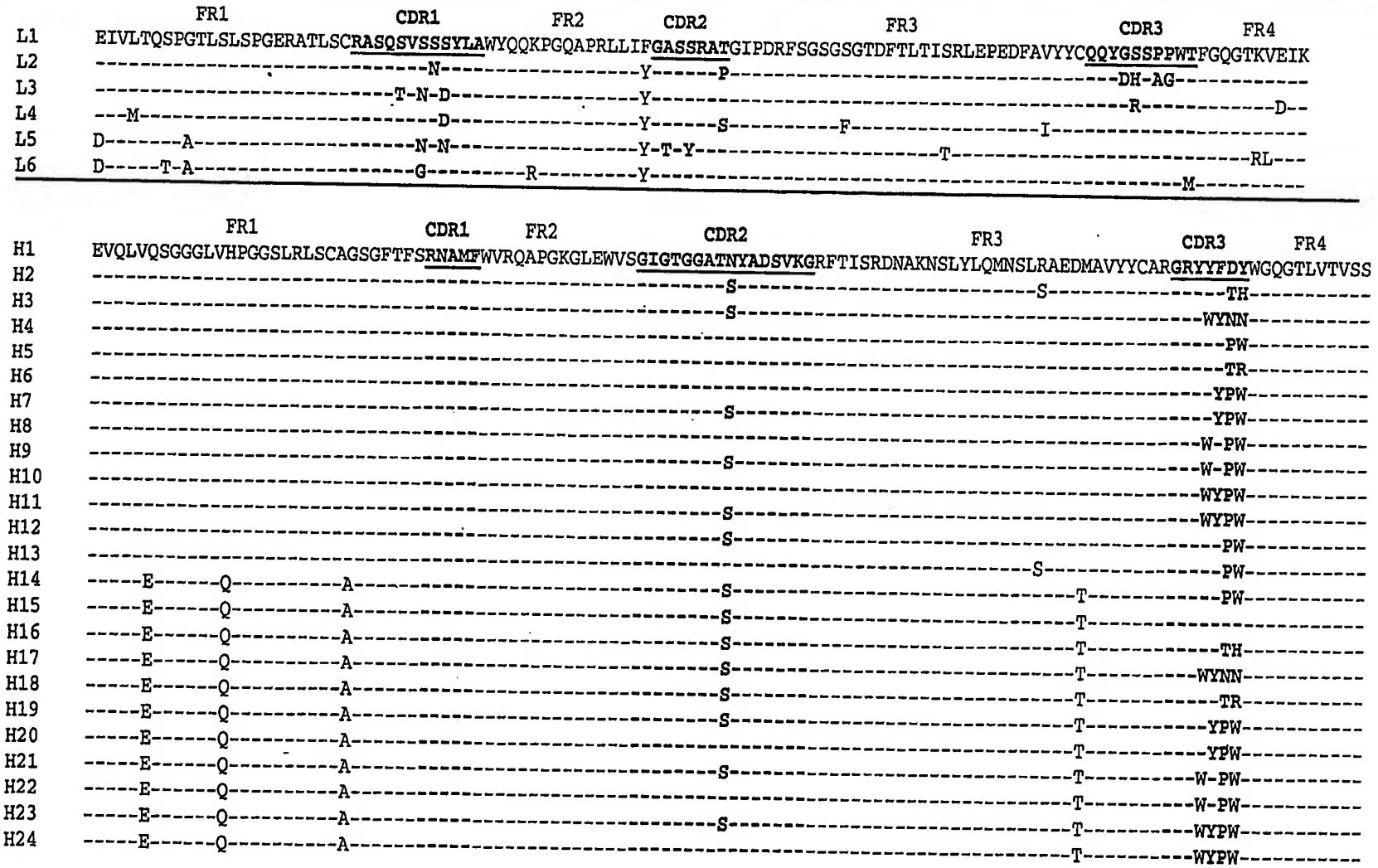
						FR3			
H1	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H2	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H3	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H4	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H5	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H6	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H7	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H8	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H9	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H10	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H11	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H12	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H13	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H14	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H15	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H16	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H17	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H18	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H19	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H20	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H21	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H22	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H23	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240
H24	181	**GACTCCGTGA**	**AGGGC**CGATT	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240

Figure 2D

H1	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H2	241	CAAATGAACA	GCCTGAGTGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H3	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H4	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H5	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H6	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H7	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H8	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H9	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H10	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H11	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H12	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H13	241	CAAATGAACA	GCCTGAGTGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H14	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H15	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H16	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H17	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H18	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H19	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H20	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H21	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H22	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H23	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300
H24	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	AGGGAGGTAC 300

		CDR3			FR4		
H1	301	TACTTTGACT	ACTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H2	301	TACTTCACCC	ACTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H3	301	TGGTACAACA	ACTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H4	301	TACTTCCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H5	301	TACTTCACGA	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H6	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H7	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H8	301	TGGTTCCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H9	301	TGGTTCCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H10	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H11	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H12	301	TACTTCCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H13	301	TACTTCCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H14	301	TACTTCCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H15	301	TACTTTGACT	ACTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H16	301	TACTTCACCC	ACTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H17	301	TGGTACAACA	ACTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H18	301	TACTTCACGA	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H19	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H20	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H21	301	TGGTTCCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H22	301	TGGTTCCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H23	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345
H24	301	TGGTACCCGT	GGTGGGGCCA	GGGAACCCTG	GTCACCGTCT	CCTCA	345

Figure 3


FR1 CDR1 FR2 CDR2 FR3 CDR3 FR4
L1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPWTFGQGTKVEIK
L2 ----------N----------Y------P----------DH-AG----------
L3 ----------T-N-D----------Y----------R----------D--
L4 ---M----------D----------Y------S----------F----------I----------
L5 D-------A----------N-N----------Y-T-Y----------T----------RL---
L6 D-----T-A----------G---------R---------Y----------M---------
FR1 CDR1 FR2 CDR2 FR3 CDR3 FR4
H1 EVQLVQSGGGLVHPGGSLRLSCAGSGFTFSRNAMFWVRQAPGKGLEWVSGIGTGGATNYADSVKGRFTISRDNAKNSLYLQMNSLRAEDMAVYYCARGRYYFDYWGQGTLVTVSS
H2 ----------S----------S----------TH----------
H3 ----------S----------WYNN----------
H4 ----------PW----------
H5 ----------TR----------
H6 ----------YPW----------
H7 ----------S----------YPW----------
H8 ----------W-PW----------
H9 ----------S----------W-PW----------
H10 ----------WYPW----------
H11 ----------S----------WYPW----------
H12 ----------S----------PW----------
H13 ----------S----------PW----------
H14 -----E------Q----------A----------S----------T----------PW----------
H15 -----E------Q----------A----------S----------T----------
H16 -----E------Q----------A----------S----------T----------TH----------
H17 -----E------Q----------A----------S----------T----------WYNN----------
H18 -----E------Q----------A----------S----------T----------TR----------
H19 -----E------Q----------A----------S----------T----------YPW----------
H20 -----E------Q----------A----------T----------YPW----------
H21 -----E------Q----------A----------S----------T----------W-PW----------
H22 -----E------Q----------A----------T----------W-PW----------
H23 -----E------Q----------A----------S----------T----------WYPW----------
H24 -----E------Q----------A----------T----------WYPW----------